

AAV Types 2 & 5 % Inhibition + Heparin (20 ug/ml)

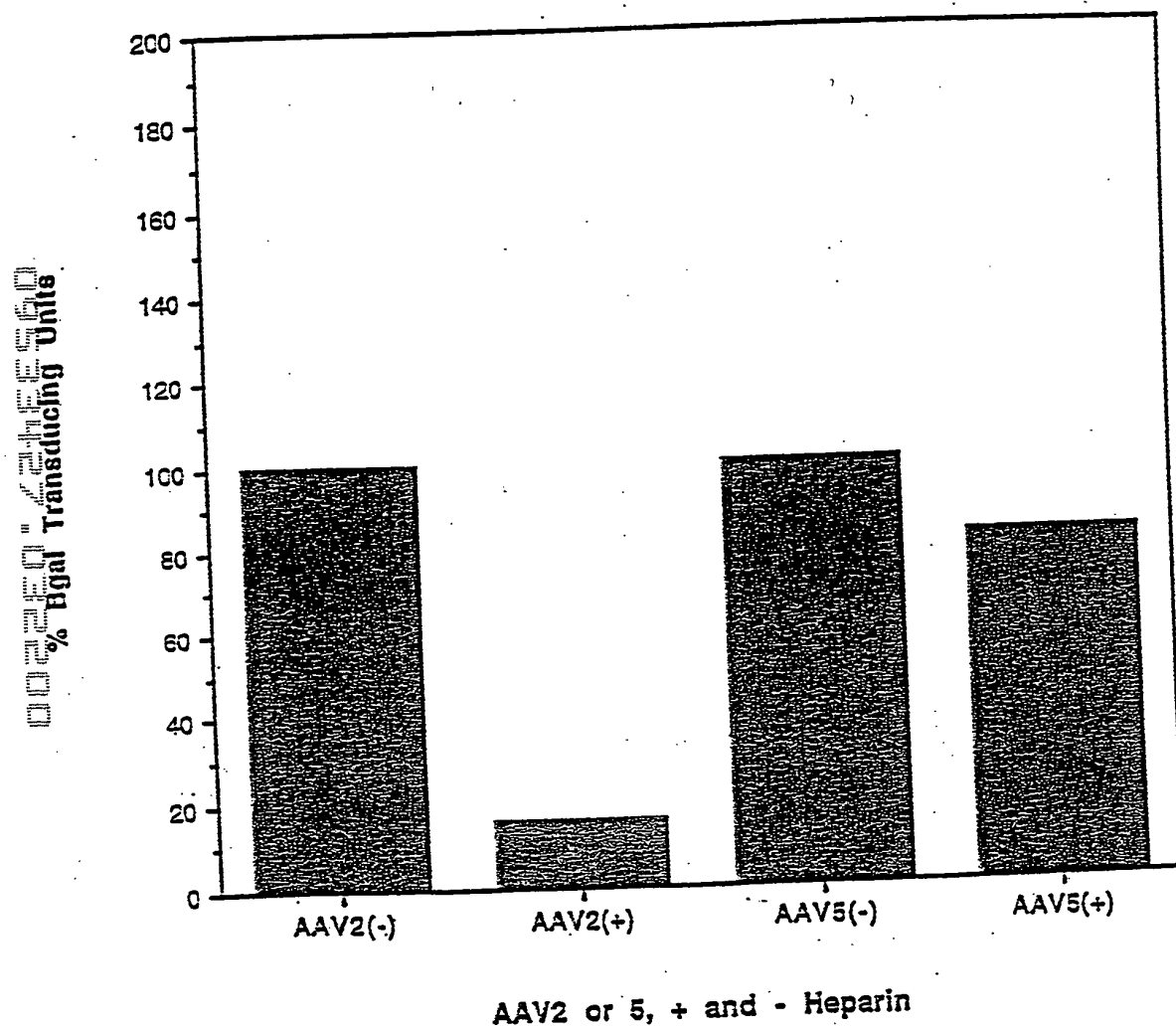
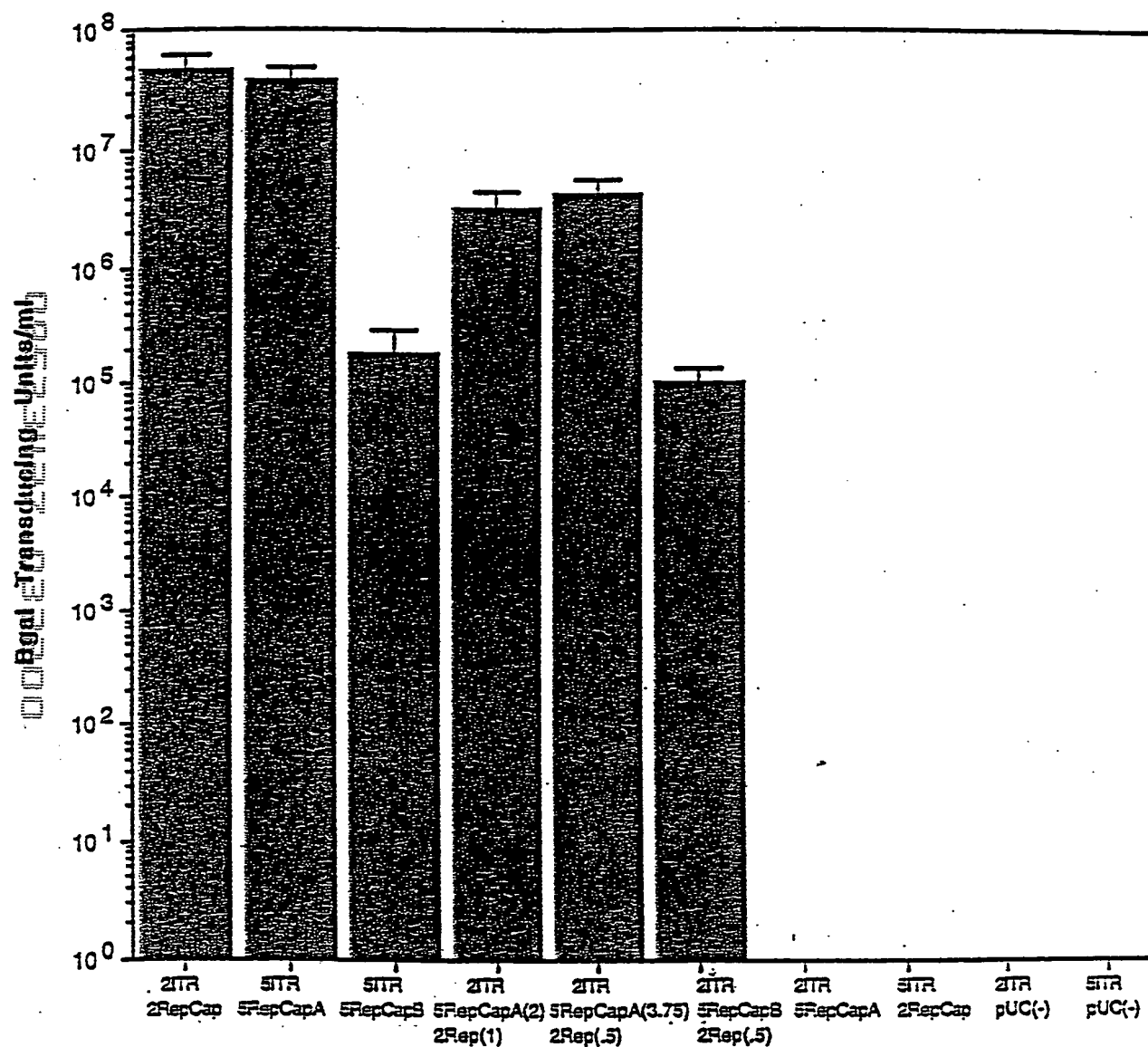


FIG. 1

AAV Types 2 & 5 Vector and Helper Plasmid Combinations



AAV2 & 5 Plasmid Combinations

FIG. 2

AAV Types 2 & 5 Tissue Tropism

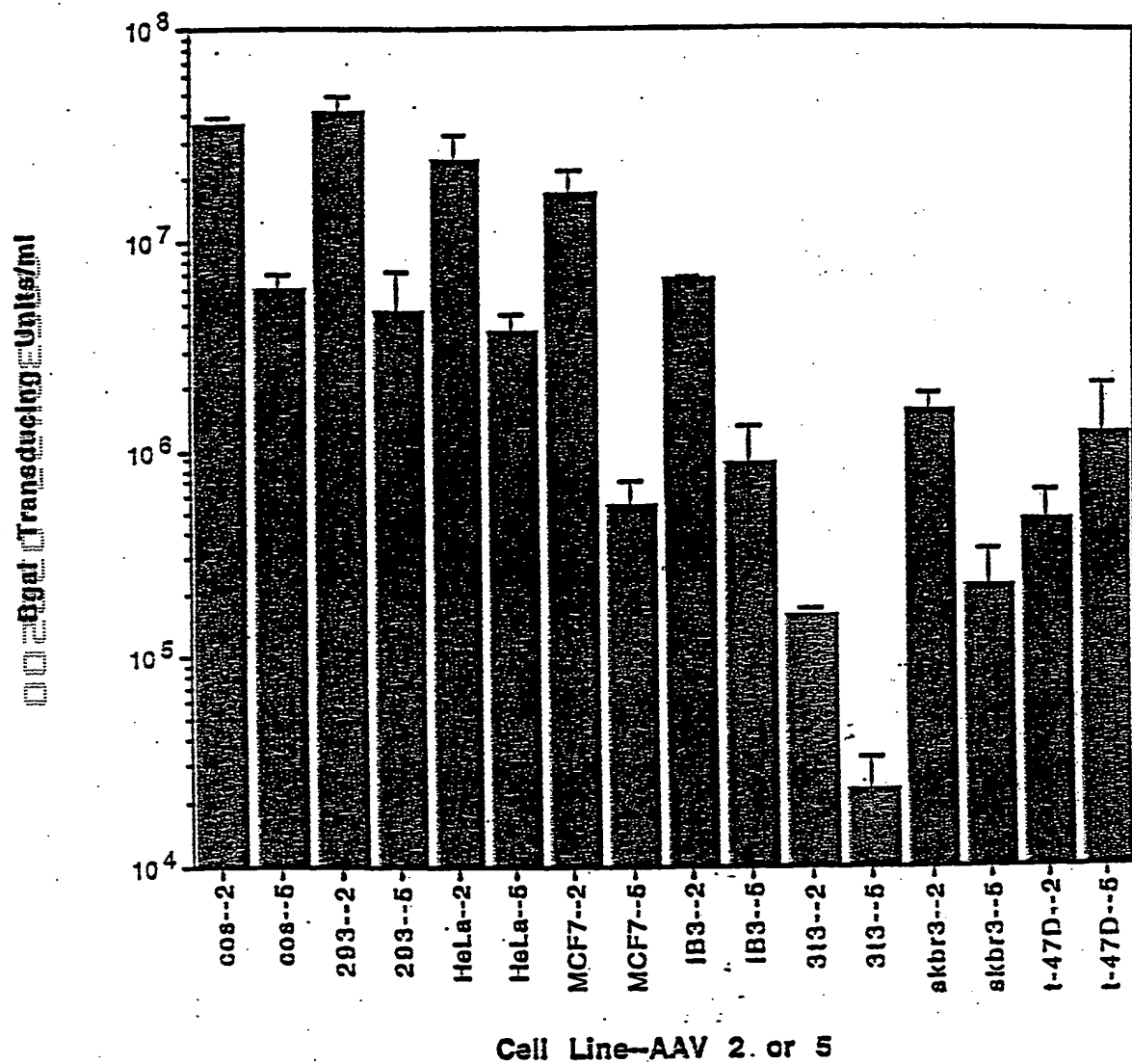


FIG. 3

 ALIGNMENT OF TWO NUCLEOTIDE SEQUENCES. *

he two sequences to be aligned are:

AV2CG.
 total number of bases: 4679.

AV5CG.
 total number of bases: 4652.

pen gap cost : 10
 nit gap cost : 12

ie character to show that two aligned residues are identical is ':'

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AV2CG - TTGGCCACTCCCTCTCTGEGCGCTCGCTCGCTCACTGA-----GGCCGGGCGA -48
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - TGGCACTCTCCCCCTGTGCGGTTGCTCGCTCGCTGCGCTCGTTTGGGGGGGTGG -55
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV2CG - C-----CAAAGGTC-GCCCGACGCCCCGGGCTTTGCCCCGG-GCGGCCTCA----- -90
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - CAGCTCAAAGAGCTGCCAGACGACGGCCCTCTGGCCGTCGCCCCCCCAAACGAGC -110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV2CG - --GTGAGCGAGCGAGCGCG-CAGAGAGG-GAGTGGCCAACTCCATCACTAGGGGT -141
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - CAGCGAGCGAGCGAACGCGACAGGGGGGAGAGTGCCACACTCTCAAGCAAGGGGG -165
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV2CG - TCCTGGAGGG-GTGGAGTCGTGACG-TGAATTACGTCATAGGGTTAGGGAGGTCC -194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - TTTTGTAAGCAGTGATGTCATAATGATGTAATGCTTATTGTCACGCGATAGTTAA -220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV2CG - TGTATTAGAGGTCACGTGA-GTGTTTTGCGACATTTTGCGACACC-----ATGT -242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - TG-ATTAACAGTCATGTGATGTGTTTTATCCAATAGGAAGAAAGCGCGGTATGA -274
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV2CG - GGTCACGCT-----GGGTATTTAAGCCCCGAGTGAGCACGCAGGGTCTCCAT -288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - GTTCTCGCGAGACTTCCGGGGTATAAAAGACCGAGTGAACGAGCCCCGC-CGCCAT -328
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV2CG - T-TTGAAGCGGGAG-GTTTGAACGCGCA-GCCGCCATGCCGGGGTTTTACGAGAT -340
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - TCTTTGCTCTGGACTGCTAGAGGACCCTCGCTGCCATGGCTACCTTCTATGAAGT -383
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV2CG - TGTGATTAAGGTCCCCAGCGACCTTGACGGGCATCTGCCCGGCATTTCTGACAGC -395
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - CATTGTTGCGCTCCCATTTGACGTGGAGGAACATCTGCCTGGAATTTCTGACAGC -438
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV2CG - TTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGG -450
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AV5CG - TTTGTGGACTGGGTAACTGGTCAAATTGGGAGCTGCCTCCAGAGTCAGATTTAA -493
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  
```

FIG. 4

AV2CG	- ATCTGAATCTGATCAGGCACCCCTGACCGTGGCCGAGAAATGCAGCGCGA	-505
AV5CG	- ATTTGACTCTGGTTGAAACAGCCTCAGTTGACGGTGGCTGATAGAATTCGCCGCGT	-548
AV2CG	- CTTTCTGACGGAATGGCGCCGTGTGAGTAAGGCCCGGAGGCCCTTTTCTTTGTG	-560
AV5CG	- GTTCCTGTACGAGTGGAACAAATTTTCCAAG---CAGGAGTCCAAATTCCTTTGTG	-600
AV2CG	- CAATTTGAGAAGGGAGAGAGCTACTTCCACATGCACGTGCTCGTGGAACACCG	-615
AV5CG	- CAGTTTGAAAAGGGATCTGAATATTTTCATCTGCACACGCTTGTGGAGACCTCCG	-655
AV2CG	- GGGTGAAATCCATGGTTTTGGGACGTTTCTGAGTCAGATTCGCGAAAACTGAT	-670
AV5CG	- GCATCTCTTCCATGGTCTCGGCCGCTACGTGAGTCAGATTCGCGCCAGCTGGT	-710
AV2CG	- TCAGAGAATTTACCGCGGGATCGAGCCGACTTTGCCAAACTGGTTCGCGGTCACA	-725
AV5CG	- GAAAGTGGTCTTCCAGGGAATTGAACCCAGATCAACGACTGGGTGCGCCATCACC	-765
AV2CG	- AAGACCAGAAATGGCGCCGGAGGCGGGAACAAGGTGGTGGATGAGTGCTACATCC	-780
AV5CG	- AAGGTAAAGAAGGGC---GGAGCC---AATAAGGTGGTGGATTCTGGGTATATTC	-814
AV2CG	- CCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATAT	-835
AV5CG	- CCGCCTACCTGCTGCCGAAGGTCCAACCGGAGCTTCAGTGGGCGTGGACAAACCT	-869
AV2CG	- GGAACAGTATTTAAGCGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCG	-890
AV5CG	- GGACGAGTATAAATTGGCCGCCCTGAATCTGGAGGAGCGCAAACGGCTCGTCGCG	-924
AV2CG	- CAGCATCTGACGCACGTGTGCGCAGACGCAGGAGCAGAACAAAGAGAATCAGAATC	-945
AV5CG	- CAGTTTCTGGCAGAATCCTCGCAG-CGCTCG--CAGGAGGCGGCTTCGCAGCGTG	-976
AV2CG	- CCAATTCTGATGCGCCGGTGATCAGATCAAAAACCTTCAGCCAGGTACATGGAGCT	-1000
AV5CG	- AGTTCTCGGCTGACCCGGTCATCAAAGCAAGACTTCCAGAAATACATGGCGCT	-1031
AV2CG	- GGTCGGGTGGCTCGTGGACAAGGGGATTACCTCGGAGAAGCAGTGGATCCAGGAG	-1055
AV5CG	- CGTCAACTGGCTCGTGGAGCACGGCATCACTTCCGAGAAGCAGTGGATCCAGGAA	-1086
AV2CG	- GACCAGGCCTCATACATCTCCTTCAATGCGGCCTCCAACTCGCGGTCCCAAATCA	-1110
AV5CG	- AATCAGGAGAGCTACCTCTCCTTCAACTCCACGGCAACTCTCGGAGCCAGATCA	-1141
AV2CG	- AGGCTGCCTTGGACAATGCGGGAAAGATTATGAGCCTGACTAAAACGCCCCCGA	-1165
AV5CG	- AGGCCGCGCTCGACAACGCGACCAAATTTATGAGTCTGACAAAAGCGCGGTGGA	-1196
AV2CG	- CTACCTGGTGGGCCAGCAGCCCGTG-GAGGACATTTCCAGCAATCGGATTTATAA	-1219
AV5CG	- CTACCTCGTGGGG-AGCTCCGTTCCCGAGGACATTTCAAAAACAGAATCTGGCA	-1250

AV2CG - AATTTTGGAACTAAACGGGTACGATCCCCAATATGCGGCTTCGGTCTTTCTGGA -1274
::: : : : : : : : : : : : : : : : :
AV5CG - AATTTTGGAGATGAATGGCTACGACCCGGCCTACGCGGGATCCATCCTCTACGGC -1305
AV2CG - TGGGCCACGAAAAAGTTCGGCAAGAGGAACACCATCTGGCTGTTTGGGCCTGCAA -1329
::: : : : : : : : : : : : : : : : :
AV5CG - TGGTGTCAGCGCTCCTTCAACAAGAGGAACACCGTCTGGCTCTACGACCCGCCA -1360
AV2CG - CTACCGGGAAGACCAACATCGCGGAGGCCATAGCCCACACTGTGCCCTTCTACGG -1384
:
AV5CG - CGACCGGCAAGACCAACATCGCGGAGGCCATCGCCACACTGTGCCCTTTTACGG -1415
AV2CG - GTGCGTAAGTGGACCAATGAGAAGTTCCTTCAACGACTGTGTGACAAGATG -1439
:
AV5CG - CTGCGTGAAGTGGACCAATGAAAAGTTCCTTTAATGACTGTGTGGACAAAATG -1470
AV2CG - GTGATCTGGTGGGAGGAGGGGAAGATGACCGCCAAGGTCGTGGAGTCGGCCAAAG -1494
:
AV5CG - CTCATTTGGTGGGAGGAGGGAAAGATGACCAACAAGGTGGTTGAATCCGCCAAGG -1525
AV2CG - CCATTCTCGGAGGAAGCAAGGTGCGCGTGGACCAGAAATGCAAGTCCTCGGCCCA -1549
:
AV5CG - CCATCCTGGGGGGCTCAAAGGTGCGGGTCGATCAGAAATGTAAATCCTCTGTTCA -1580
AV2CG - GATAGACCCGACTCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATT -1604
:
AV5CG - AATTGATTCTACCCCTGTCATTGTAAGTTCCTCAATAACAACATGTGTGTTGGTGGTG -1635
AV2CG - GACGGGAACTCAACGACCTTCGAACACCAGCAGCCGTTGCAAGACCGGATGTTCA -1659
:
AV5CG - GATGGGAATTCCACGACCTTTGAACACCAGCAGCCGCTGGAGGACCGCATGTTCA -1690
AV2CG - AATTTGAACTCACCCGCCGTCTGGATCATGACTTTGGGAAGGTCACCAAGCAGGA -1714
:
AV5CG - AATTTGAACTGACTAAGCGGCTCCCGCCAGATTTTGGCAAGATTACTAAGCAGGA -1745
AV2CG - AGTCAAAGACTTTTTTCCGGTGGGCAAAGGATCACGTGGTTGAGGTGGAGCATGAA -1769
:
AV5CG - AGTCAAGGACTTTTTTGCTTGGGCAAAGGTCAATCAGGTGCCGGTGAATCACGAG -1800
AV2CG - TTCTACGTCAAAAAGGG--TGGAGCCAAGAAAAGACCCGCCCCCAGTGACGCAGA -1822
:
AV5CG - TTTAAAGTTCCAGGGAATTGGCGGGAAGTAAAGGGGCG-----GAGAAATCTC -1849
AV2CG - TATAAGTGAGCCCAAACGGGTGCGCGAGTCAGTTGCGCAGCCATCGACGTCAGAC -1877
:
AV5CG - TAAAAC---GCCCACT-GGGTGA-CGTCACCAATACT-AGCTATAAAAGTCTGGA -1898
AV2CG - GCGBAAGCTTCGATCAACTACGCAGACAGGTACAAAACAAAT-GTTCTCGTCAC -1931
:
AV5CG - G---AAGC--GGGCCAGGCTCTCATTT-GTTCCCGAGACGCCTCGCAGTTTCAGAC -1947
AV2CG - GTGGGCATGAATCT-GATGCTGTTTCCCTGCAGACAATGCGAGAGAATGAATCAG -1985
: :

AV5CG	- GTGACTGTTGATCCTCCTCTGCGACCGCTCA-ATTGGAACAAGGTAT--G	-1999
AV2CG	- AATTCAAATATCTGCTTCACTCACGGACAGAAAGACTGTTTAGAGTGCTTCCCG	-2040
AV5CG	- ATTGCAAATG--TGACT-A-TCATGCTCAATTGACA---ACATTTCTAACAAA	-2046
AV2CG	- TGTCA-GAATCTCAACCCGTTTCTGTCGTCAAAAAGGC--GTATCAGAACTGTG	-2092
AV5CG	- TGTGATGAATGTGAATATTTGAATCGGGGCAAAAATGGATGTATCTGTCACAATG	-2101
AV2CG	- CTACATTCA-TCATAT----CATGGGAAAGGTGCCAGACGCTTGCACTGCCTGCG	-2142
AV5CG	- TAACTCACTGTCAAATTTGTCTATGGGATTCCTCCCTGGGAAAAGGAAAAGTTG--	-2154
AV2CG	- ATCTGGTCAATGTGGATTTGGATGACTGCATCTTTGAACAATAAATGATTTAAAT	-2197
AV5CG	- -TCAGATTT-TGGGGATTTTGACGATGCCAATAAAGAACAGTAAATAAAGCGAGT	-2207
AV2CG	- CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGA	-2252
AV5CG	- -AGTCATGTCTTTTGTGATCACCCTCCAGATTGGTTGGAAGAAGTTGG---TGA	-2258
AV2CG	- AGGAATAAGACAGTGGTGGAGCTCAAACCTGGCCCACCACCACCAAAGCCCGCA	-2307
AV5CG	- AGGTCTTCGCGAGTTTTTTGGGCCTTGAAGCGGGCCCACCGAAACCAAACCCAAT	-2313
AV2CG	- GAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCTTCCTGGGTACAAGTACCTCG	-2362
AV5CG	- CAGCAGCATCAAGATCAAGCCCGTGGTCTTGTGCTGCCTGGTTATAACTATCTCG	-2368
AV2CG	- GACCCTTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAGACGCCGCGGC	-2417
AV5CG	- GACCCGGAAACGGTCTCGATCGAGGAGAGCCTGTCAACAGGGCAGACGAGGTCGC	-2423
AV2CG	- CCTCGAGCACGACAAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTAC	-2472
AV5CG	- GCGAGAGCACGACATCTCGTACAACGAGCAGCTTGAGGCGGGAGACAACCCCTAC	-2478
AV2CG	- CTCAAGTACAACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGT	-2527
AV5CG	- CTCAAGTACAACCACGCCGACGCCGAGTTTCAGGAGAAGCTCGCCGACGACACAT	-2533
AV2CG	- CTTTTGCGGGCAACCTCGGACGAGCAGTCTTCCAGGCGAAAAAGAGGGTTCTTGA	-2582
AV5CG	- CCTTCGGGGGAAACCTCGGAAAGGCAGTCTTTCAGGCCAAGAAAAGGGTTCTCGA	-2588
AV2CG	- ACCTCTGGGCCTGGTTGAGGAACCTGTTAAGACGGCTCCGGGAAAAAAGAGGCCG	-2637
AV5CG	- ACCTTTTGGCCTGGTTGAAGAGGGTGCTAAGACGGCCCCTACCGGAAAGCGGATA	-2643
AV2CG	- GTAGAGCACTCTCCTGTGGAGCCAGACTCCTCCTCGGGAAACCGGAAAGGCGGGCC	-2692
AV5CG	- GACGACCACTTTCCAAAA-AGAAAGAAGGCTC---GGA-CCGAAGAGGACT-CC	-2691
AV2CG	- AGCAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGACGCAG-ACTCAG	-2746

AV5CG - A--AGCCTTCCACC-----TCGTCAGAC-GCCGAAGCTGGACCCAG -2729
 AV2CG - TACCTGACCCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAAC -2801
 AV5CG - ---CGGATCCC-AGCAGCTGCAAATCCCAGCCCAACCAGCCTCAAGTTTGGGAGC -2780
 AV2CG - TAATACGATGGCTACAGGCAGTGGCGCACCAATGGCAGACAATAACGAGGGCGCC -2856
 AV5CG - TGATACAATGTCTGCGGGAGGTGGCGGCCCATTTGGGCGACAATAACCAAGGTGCC -2835
 AV2CG - GACGGAGTGGGTAATTCCTCGGGAAATTGGCATTGCGATTCCACATGGATGGGCG -2911
 AV5CG - GATGGAGTGGGCAATGCCTCGGGAGATTGGCATTGCGATTCCACGTGGATGGGGG -2890
 AV2CG - ACAGAGTCATCACCACCAGCACC CGAACCTGGGCCCTGCCACCTACAACAACCA -2966
 AV5CG - ACAGAGTCGTCACCAAGTCCACCCGAACCTGGGTGCTGCCCAGCTACAACAACCA -2945
 AV2CG - CCTCTACAAACAAATTTCCAGCCAATCAGGAGGCTCGA---ACGACAATCACTAC -3018
 AV5CG - CCAGTACCGAGAGATCAAAGCGGCTCCGTCGACGGAAGCAACGCCAACGCCTAC -3000
 AV2CG - TTTGGCTACAGCACCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACT -3073
 AV5CG - TTTGGATACAGCACCCTTGGGGGTACTTTGACTTTAACCGCTTCCACAGCCACT -3055
 AV2CG - TTTACCACGTGACTGGCAAAGACTCATCAACAACAACTGGGGATTCCGACCCAA -3128
 AV5CG - GGAGCCCCCGAGACTGGCAAAGACTCATCAACAATACTGGGGCTTCAGACCCCG -3110
 AV2CG - GAGACTCAACTTCAAGCTCTTTAACATTCAAGTCAAAGAGGTCACGCAGAATGAC -3183
 AV5CG - GTCCCTCAGAGTCAAATCTTCAACATTCAAGTCAAAGAGGTCACGGTGCAGGAC -3165
 AV2CG - GGTACGACGACGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGACT -3238
 AV5CG - TCCACCACCACCATCGCCAACAACCTCACCTCCACCGTCCAAGTGTTTACGGACG -3220
 AV2CG - CGGAGTACCAGCTCCCGTACGTCCTCGGCTCGGCGCATCAAGGATGCCTCCCGCC -3293
 AV5CG - ACGACTACCAGCTGCCCTACGTCGTCGGCAACGGGACCGAGGGATGCCTGCCGGC -3275
 AV2CG - GTTCCCAGCAGACGTCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAAC -3348
 AV5CG - CTTCCCTCCGCAGGTCTTTACGCTGCCGCAGTACGGTTACGCGACGCTGAACCGC -3330
 AV2CG - GGGAGT-CAGGCAGTAGGAC---GCTCTTCA--TTTACTGCCTGGAGTACTTTC -3397
 AV5CG - GACAACACAGAAAATCCCACCGAGAGGAGCAGCTTCTTCTGCCTAGAGTACTTTC -3385
 AV2CG - CTTCTCAGATGCTGCGTACCGGAAACAACCTTACCTTCAGCTACACTTTTGAGGA -3452
 AV5CG - CCAGCAAGATGCTGAGAACGGGCAACAACCTTTGAGTTTACCTACAACCTTTGAGGA -3440

AV2CG	- CGTTCCTTTCCACAAGCTACGCTCACAGCCAGAGTCTGGACCTCTCATGAAT	-3507
AV5CG	- GGTGCCCTTCCACTCCAGCTTCGCTCCAGTCAGAACCTGTTCAAGCTGGCCAAC	-3495
AV2CG	- CCTCTCATCGACCAGTACCTGTATTACTT---GAGCAGAACAACACTC-----	-3553
AV5CG	- CCGCTGGTGGACCAGTACTTGTACCGCTTCGTGAGCACAAATAACACTGGCGGAG	-3550
AV2CG	- -CAAGTGGAAACCACCAC---GCAGTCA-AGGCTTCAGTT--TTCTCAGGCCGGAG	-3601
AV5CG	- TCCAGTTCAACAAGAACCTGGCCGGGAGATACGCCAACACCTACAAAACTGGTT	-3605
AV2CG	- CGAGTGACATTCTGGGACCAGTCTAGGAACTGGCTTCCTGGACCCTGTTACCGCCA	-3656
AV5CG	- CCCGGGGCCCATGGGCCGAACCCAGGG-CTGGAA-CCTGGGCTCCGGGGTCAACC	-3658
AV2CG	- GCAGCGAGTATCAAAGACATCTGCGGATAACAACAACAGTGAATACTCGTGGACT	-3711
AV5CG	- GC-GCCAGTGTCTAGCGCCTTC-GCCACGACCAATAGGA-TGGAG-CTCGAGGGCG	-3709
AV2CG	- GGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGG	-3766
AV5CG	- CGAGTTACCAGGTGCCCCCGCA---GCCGA-ACGGCATGACCAACAACCTCCAGG	-3760
AV2CG	- CCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCTCAGAGCGGGGTCT	-3821
AV5CG	- GCA--GCAA--CACCTATGCCCTGGAGAACACTATGATCTTCAA--CAG---C-	-3804
AV2CG	- CATCTTTGGGAAGCAAGGCTCAGAGAAAACAAATGTGGACATTGAAAAGGTCATG	-3876
AV5CG	- CAGCCG-GCGAACC CGGCACCACCGCCACGTACCTCGAGGGCAACATGCTCATC	-3858
AV2CG	- ATTACAGACGAAGAGGAAATCAGGACAACCAATCCCGTGGC-TACGGAGCAGTAT	-3930
AV5CG	- AC--CAG-CGAGAGCGAGACGCAGCCGGTGAACCGCGTGGCGTACAACGTCGGCG	-3910
AV2CG	- GGTTCGTATCTACCAACCTCCAGAGAGGCAACAGACAAGCAGCTACCGCAGATG	-3985
AV5CG	- GGCAGA-TGGCCACCAACAACCAGAGCTCCACCACTGCCCCCGCAGCCGGCACGT	-3964
AV2CG	- TCAACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCT	-4040
AV5CG	- ACAACCTCCAGGAAATCGTGCCCGGCAGCGTGTGGATGGAGAGGGACGTGTACCT	-4019
AV2CG	- TCAGGGGCCCCTCTGGGCAAAGATTCCACACACGGACGGACATTTTCACCCCTCT	-4095
AV5CG	- CCAAGGACCCATCTGGGCCAAGATCCAGAGACGGGGGCGCACTTTCACCCCTCT	-4074
AV2CG	- CCCCTCATGGGTGGATTCTGGACTTAAACACCCTCCTCCACAGATTCTCATCAAGA	-4150
AV5CG	- CCGGCCATGGGCGGATTCTGGACTCAAACACCCACCGCCCATGATGCTCATCAAGA	-4129
AV2CG	- ACACCCCGGTACCTGCGAATCCTTCGACCACCTTCAGTG-CGGCAAAGTTTGCTT	-4204
AV5CG	- ACACGCCTGTGCCCGGAAATA--TC-ACCAGCTTCTCGGACGTGCCCGTCAGCAG	-4181

FIG. 5

=PALIGN

=PC / GENIE

 * ALIGNMENT OF TWO PROTEIN SEQUENCES. *

TRIG. AC 4

DE VP1

Total num

OS AAVZ
Total number of residues: 735.

DE AAV

Total number

Comparison matrix : Structure-genetic matrix.

Open gap cost : 8

Unit gap cost : 5

The character to show that two aligned residues are identical is ':'

The character to show that two aligned residues are similar is:

The character to show that two aligned residues are similar is the BLOSUM62 matrix. Amino acids said to be 'similar' are: A,S,T; D,E; N,Q; R,K; I,L,M,V; F,Y,W

AAV2VP1	-	MAADGYLPDWLEDTLSEGIQWWKLKPGPPPKPAERHKDDSRGLVLPGYKYLG	-55
AAV5VP1	-	MSFVDHPPDWLEE-VGEGLREFLGLLEAGPPKPKPNQQHQDQARGLVLPGYNYLG	-54
AAV2VP1	-	FNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADA EFQERLKEDTSF	-110
AAV5VP1	-	GNGLDRGEPVNRADDEVAREHDISYNEQLEAGDNPYLKYNHADA EFQEKLADDTSF	-109
AAV2VP1	-	GGNLGRAVFOAKKRVLEPLGLVEEPVKTPAGKKRPVEHSPVEPDSSSGTGKAGQQ	-165
AAV5VP1	-	GGNLGKAVFOAKKRVLEPFGLVEEGAKTAPTGKRIDDHFPKR--KKARTEEDSKP	-162
AAV2VP1	-	PARKRLNFGQTDGADSVDPDQPLGQPPAAPSGLGTNTMATGSGAPMADNNEGADG	-220
AAV5VP1	-	STS-----SDAEAGPSGSQQLQIPAQPASSLGADTMSAGGGGPLGDNNQGADG	-210
AAV2VP1	-	VGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQISSQSG-ASNDNHYFG	-274
AAV5VP1	-	VGNASGDWHCDSTWMGDRVVTKSTRTWVLPSSYNNHQQYREIKSGSVDGSNANAYFG	-265
AAV2VP1	-	YSTPWGYFDFNRFHCHFSRPDWQRLINNNWGFPRPKRLNFKLFNIQVKEVTQNDGT	-329
AAV5VP1	-	YSTPWGYFDFNRFHSHWSRPDWQRLINNYWGFPRPSLRVKIFNIQVKEVTVQDST	-320
AAV2VP1	-	TTIANNLSTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNGS	-384
AAV5VP1	-	TTIANNLSTSTVQVFTDDDYQLPYVVGNGTEGCLPAFPQVFTLPQYGYATLNRDN	-375

AAV2VP1 - Q--AVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPL -437
 AAV5VP1 - TENPTERSSFFCLEYFPSKMLRTGNNFEFTYNFEEVPFHSSFAPSQNLFKLANPL -430
 AAV2VP1 - IDQYLYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTS -492
 AAV5VP1 - VDQYLYRFVSTNNTGG-----VQFNKNLAGRYANTYKNWFPGPMGRTQGWNLGS -479
 AAV2VP1 - ADNNSSEYSWTGATKYHLNGRDSLVPNGPAMASHKDDEEKFFPQSGVLIFGKQGS -547
 AAV5VP1 - GVNRAVSASFATTNRMELEGASYQVPQPNGMTNNLQGSNTYALENTMIFNSQPA -534
 AAV2VP1 - EKTNVDI---EKVMITDEEEIIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQG -599
 AAV5VP1 - NPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQE -589
 AAV2VP1 - VLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPMLGGFGLKHPPPOILIKNTPVP -654
 AAV5VP1 - IVPGSVWMERDVYLQGPWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVP -644
 AAV2VP1 - ANPSTTFSAKFASFITQYSTGQVSVEIEWELQKENS KRWNPEIQYTSNYNKS VN -709
 AAV5VP1 - GNI-TSFSDVPVSSFITQYSTGQVTVEMEWELKKENS KRWNPEIQYTNNYNDPQF -698
 AAV2VP1 - VDFTVDTNGVYSEPRPIGTRYLTRNL -735
 AAV5VP1 - VDFAPDSTGEYRTRPIGTRYLTRPL -724

Identity : 421 (58.15%)

Similarity: 63 (8.70%)

Number of gaps inserted in AAV2VP1: 3

Number of gaps inserted in AAV5VP1: 5

==22-JAN-1997==PALIGN==PC/GENE==

FIG. 6

31-DEC-1996

PC/GENE

* ALIGNMENT OF TWO PROTEIN SEQUENCES. *

The two sequences to be aligned are:

REP78.
DE REP78
OS AAV
Total number of residues: 621.

AAV5REP.
DE REP
OS AAV5
Total number of residues: 610.

Comparison matrix : Structure-genetic matrix.
Open gap cost : 8
Unit gap cost : 5

The character to show that two aligned residues are identical is ':'
The character to show that two aligned residues are similar is '.'
Amino acids said to be 'similar' are: A,S,T; D,E; N,Q; R,K; I,L,M,V; F,Y,W

REP78	-	MPGFYEIVIKVPSDL DGHLPGISDSFVNWVAEKEWELPPDSMDLNLIEQAPLTV	-55
AAV5REP	-	MATFYEVIVRVFPDVEEHLPGISDSFVDWVTGQIWELPPESDLNLTVEQPQLTV	-55
REP78	-	AEKLQORDFLTEWRRVSKAPEALFFVQFEKGESYFHMVVLVETTGVKSMVLGRFLS	-110
AAV5REP	-	ADRIRRVFLYEWNKFSKQ-ESKFFVQFEKGSEYFHLHTLVETSGISSMVLGRYVS	-109
REP78	-	QIREKLIQRIYRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPEL	-165
AAV5REP	-	QIRAQLVKVVFQIEPQINDWVAITKVKKG--GANKVVD SGYIPAYLLPKVQPEL	-162
REP78	-	QWAWTNMEQYLSACLNLTERKRLVAQHLTHVSQTQEONKENQNPNSDAPVIRSKT	-220
AAV5REP	-	QWAWTNLDEYKLAALNLEERKRLVAQFLA-ESSQRSQEAASQREFSADPVIKSKT	-216
REP78	-	SARYMELVGWLVDKGITSEKQWIQEDQASYISFNAASNRSQIKAALDNAGKIMS	-275
AAV5REP	-	SQKYMALVNWLVEHGITSEKQWIQENQESYLSFNSTGNSRSQIKAALDNATKIMS	-271
REP78	-	LTKTAPDYL VGQQPVEDISSNRIYKILELNGYDPQYAA SVFLGWATKKFGKRNTI	-330
AAV5REP	-	LTKSAVDYL VGSSVPEDISKNRIWQIFEMNGYDPAYAGSILYGWCQRSFNKRNTV	-326
REP78	-	WLFGPATTTGKTNIAEAIAHTVPFYGCVNWTNENFPFND CVDKMWIWWEEGKMTAK	-385
AAV5REP	-	WLYGPATTTGKTNIAEAIAHTVPFYGCVNWTNENFPFND CVDKMLIWWEEGKMTNK	-381

REP78 - VVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFEHQQP -440
 AAV5REP - VVESAKAILGGSKVRVDQKCKSSVQIDSTPVIVTSNTNMCVVVDGNSTTFEHQQP -436
 REP78 - LQDRMFKFELTRRLDHDGKVTQEVKDFFRWAKDHVVEVEHEFYVKKGGAKKRP -495
 AAV5REP - LEDRMFKFELTKRLPPDFGKITKQEVKDFFAWAKVNQVPVTHEFKVPRELAGTK- -490
 REP78 - APSDADISEPKRVRESVAQPSTSDAEASINYADRYQNKCSREHVGMLMLFFCRQC -550
 AAV5REP - GAEKSLKRPLGDTVNTXYKSLEKRARLSFVPETPRSSDVTVDPAPLRPLNWNTRY -545
 REP78 - ERMNONSNICFTHGQKDCLECFVSESQPVSVVKKAYQKLCYIHHIMGKVPDACT -605
 AAV5REP - DC-KCDYHAQFDNISNKCDECEYLNRGKNGCICHNVTH-CQICHGIPPWEKENLS -598
 REP78 - ACDLVNVLDLDDCIFEQ -621
 AAV5REP - DF----GDFDDANKEQ -610

Identity : 355 (58.2%)

Similarity: 56 (9.2%)

Number of gaps inserted in REP78: 0

Number of gaps inserted in AAV5REP: 7

31-DEC-1996

PC/GENE

002200

Apical transduction of human airway epithelia with rAAV2 and rAAV5

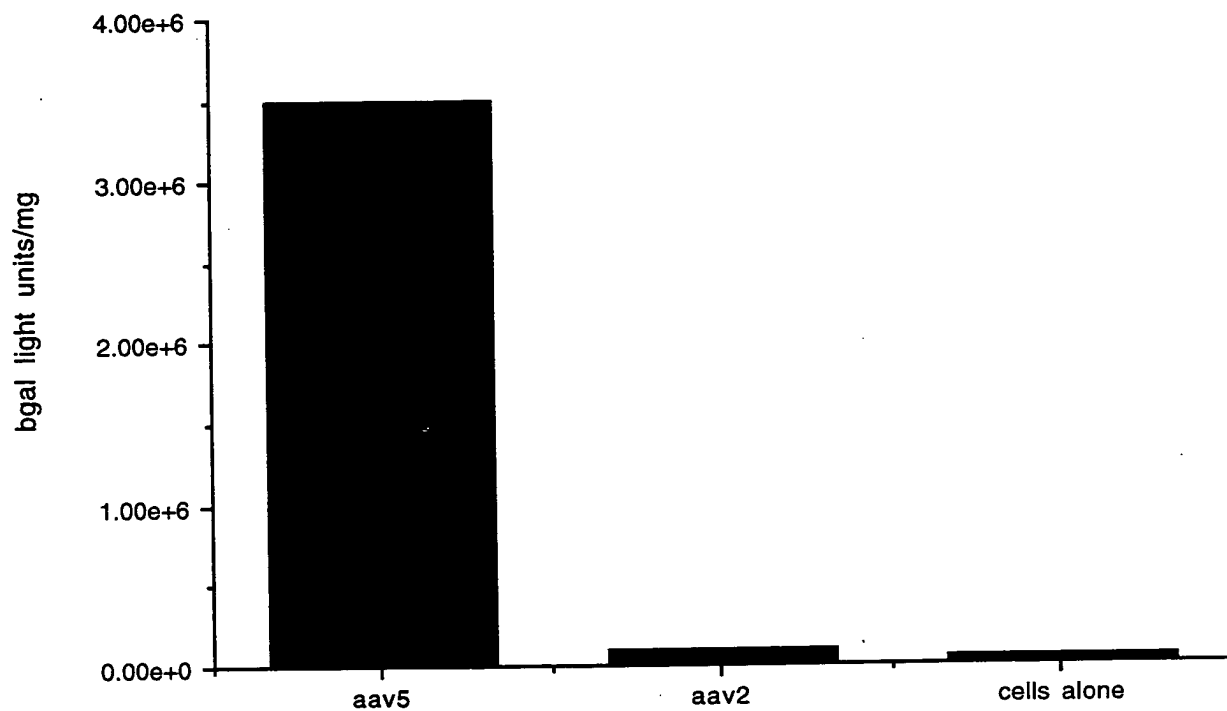


FIG. 7

002250" 24E560

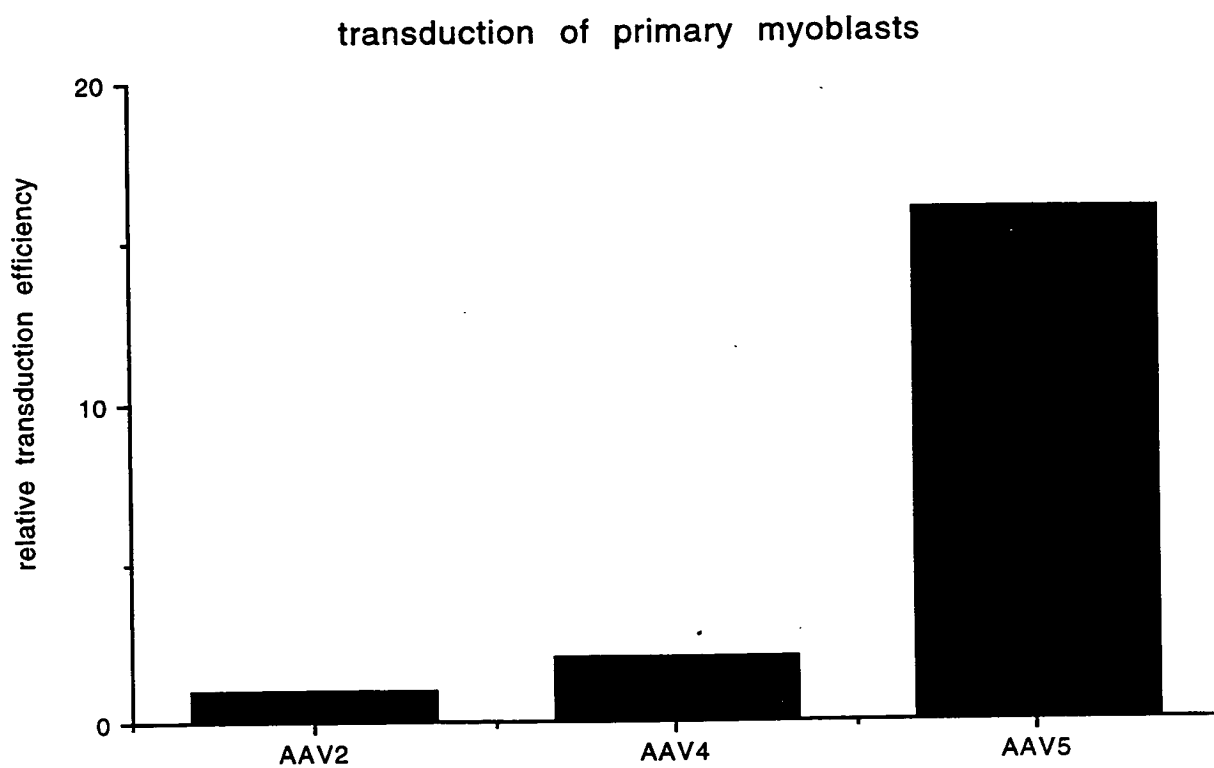


FIG. 8

AAV5 Primary Rat Brain Explant

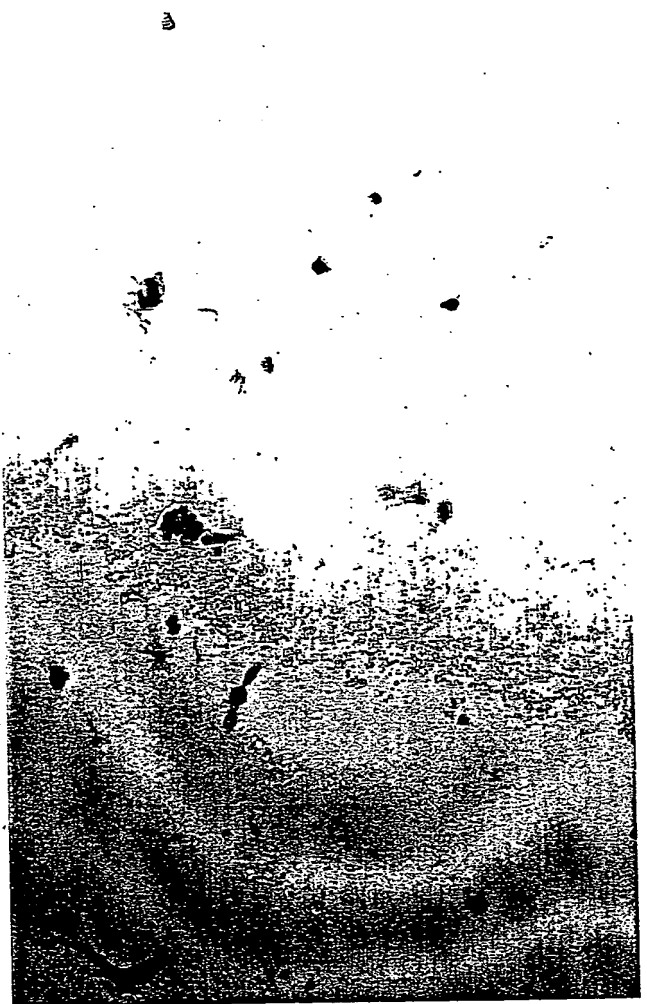


FIG. 9

09533427.032200

HUVEC

TAHV2

TAHV5



FIG. 10

09533427.032200

0022280" 24E560

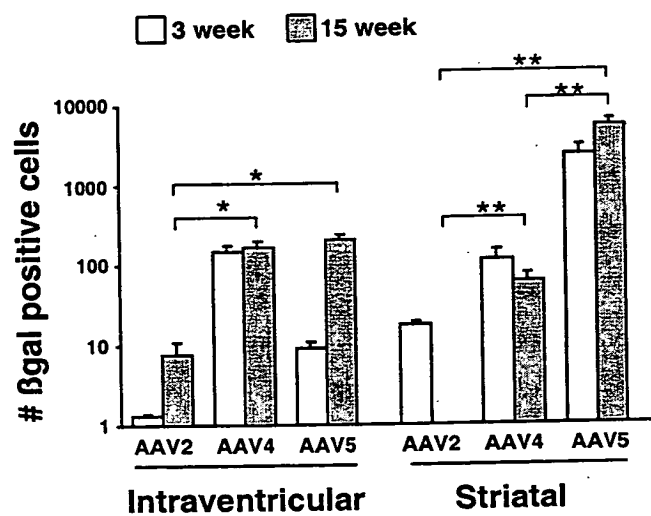


Fig. 11

002220" 24000560

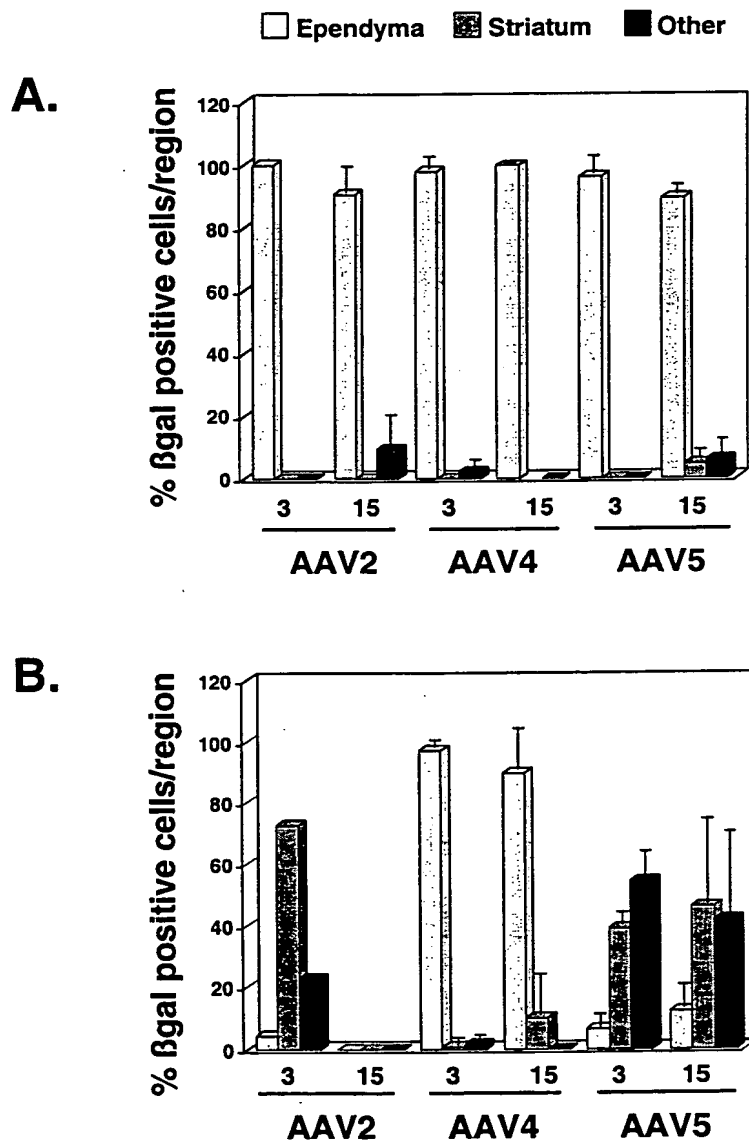


Fig. 12

002220 224E560

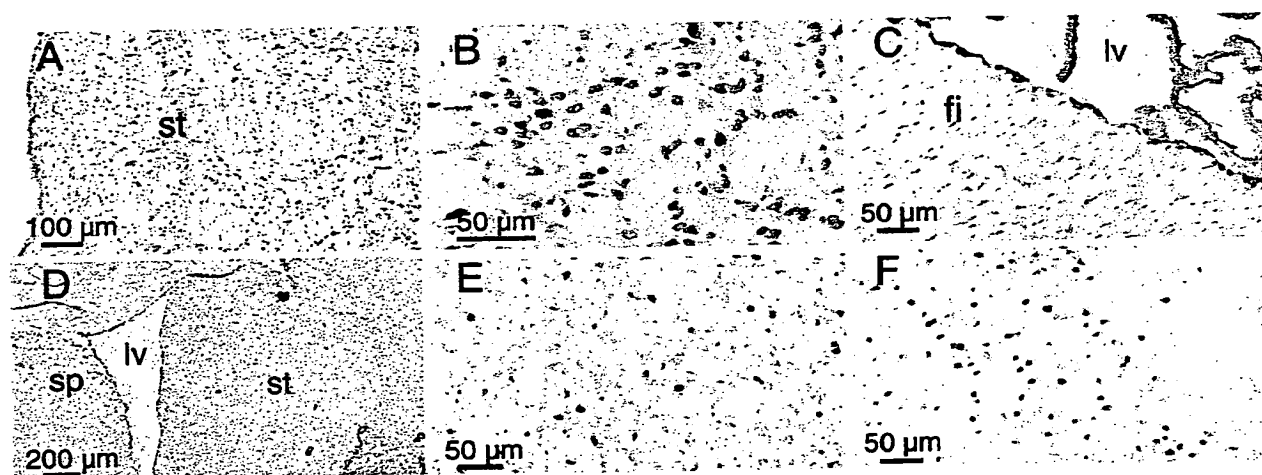


Fig. 13

09533427-032200

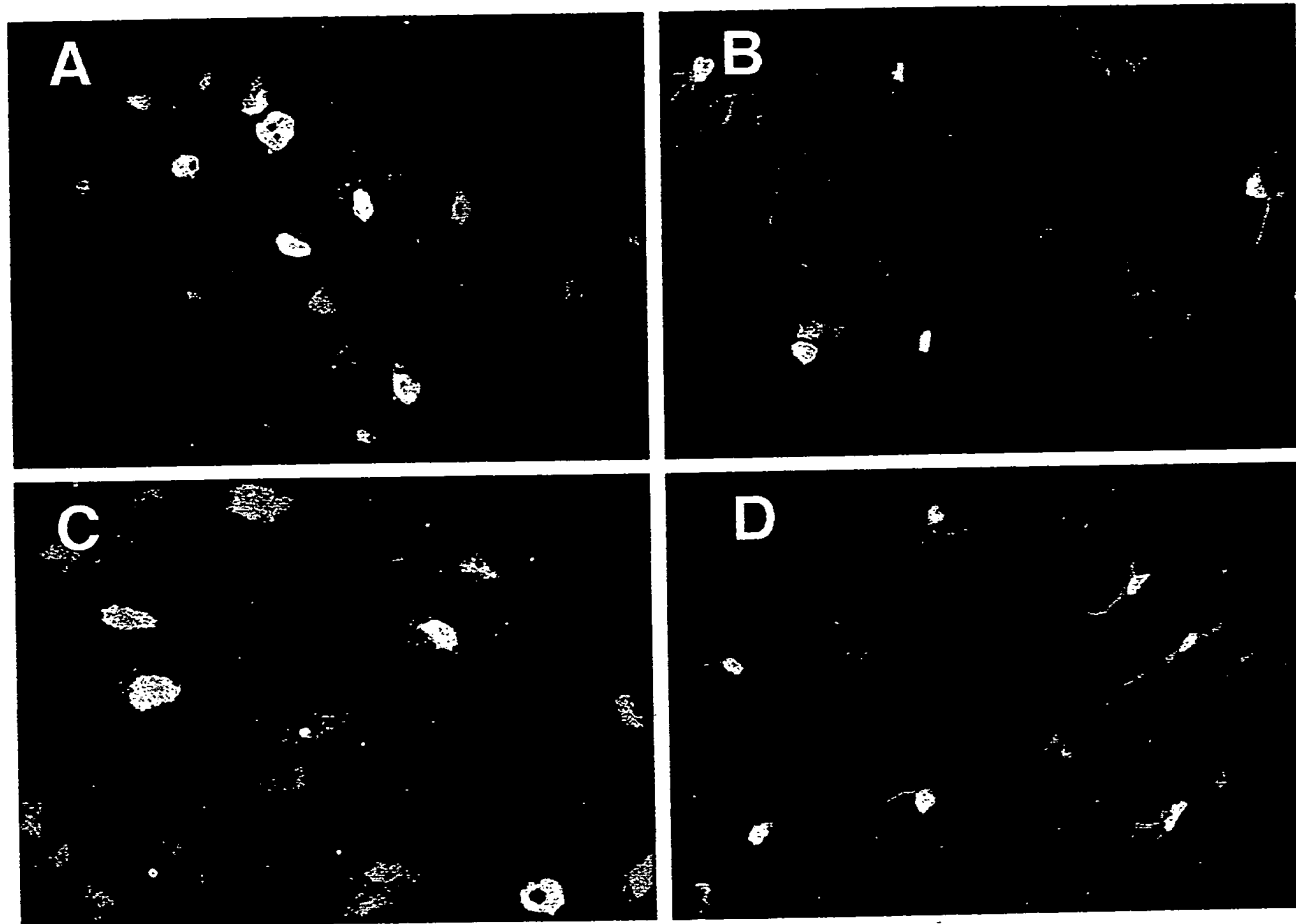


Fig. 14

002220" / 24EES60

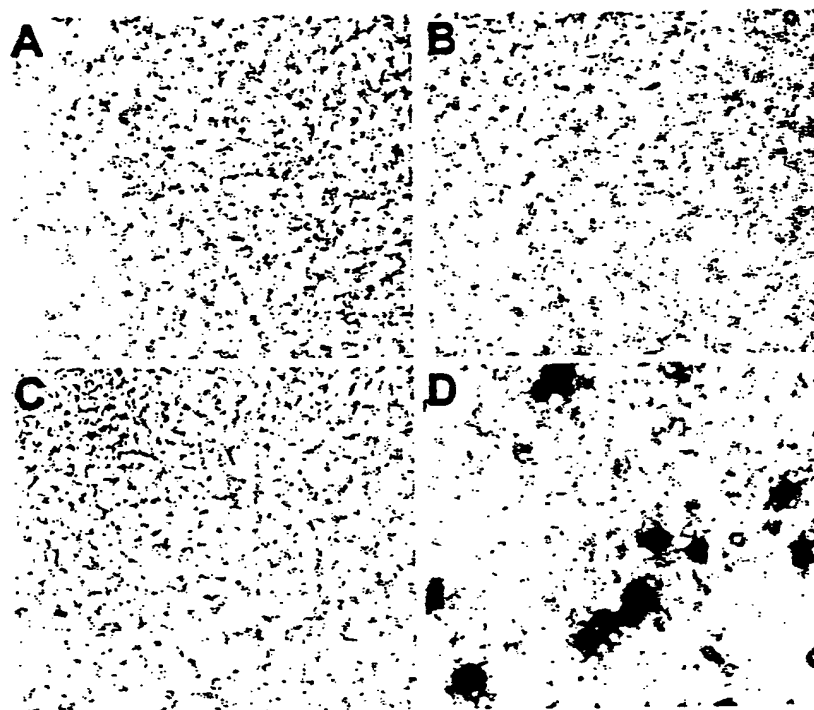


Fig. 15

09533427 032200

E

βGal Activity
(L.U./mgx10⁶)

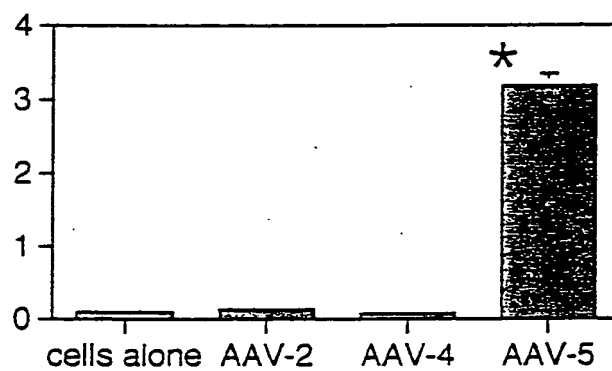
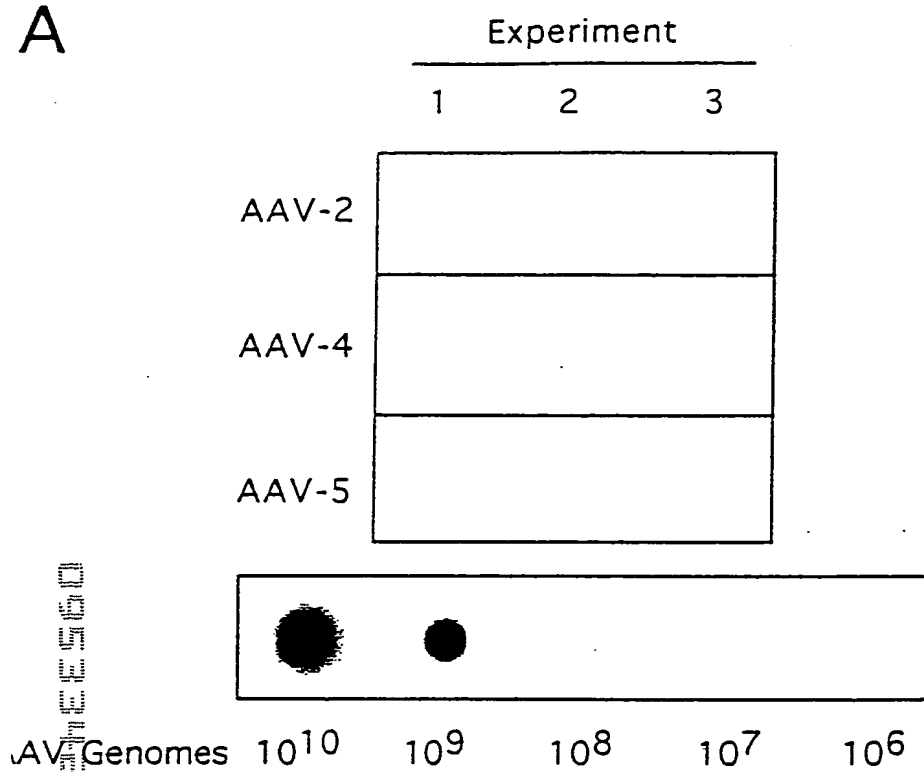


Fig. 1b A

A



B

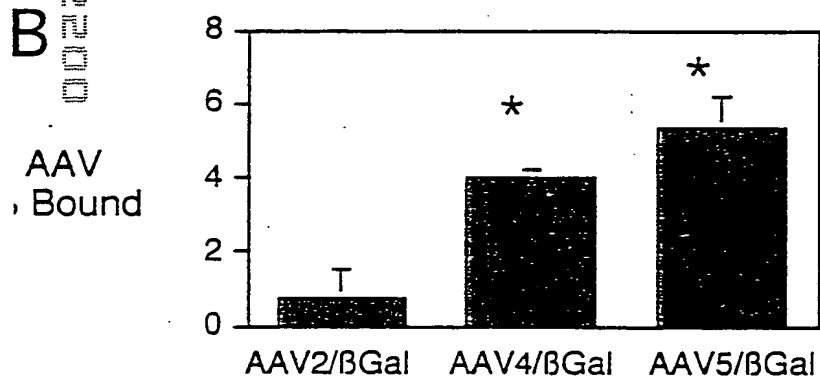


Fig. 16B

002250" 24E5560

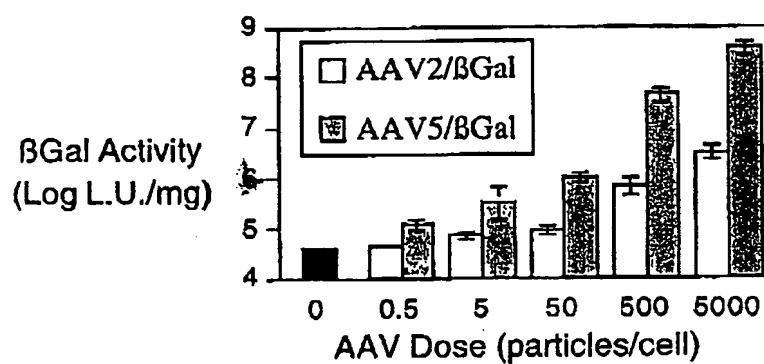


Fig. 17

00220" 224E560

β Gal Activity
(L.U./mgx10⁶)

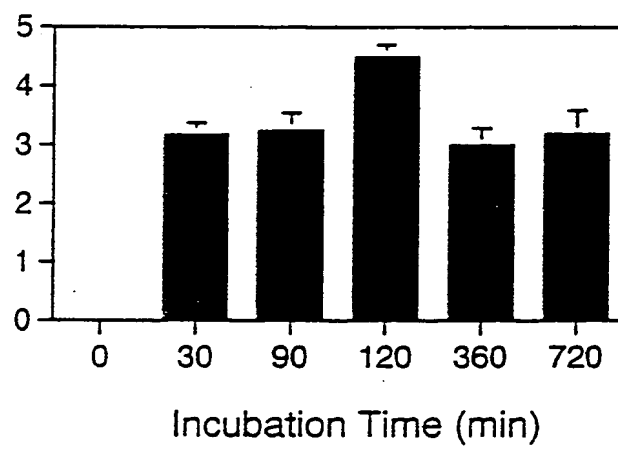


Fig 18

002220 "22422200

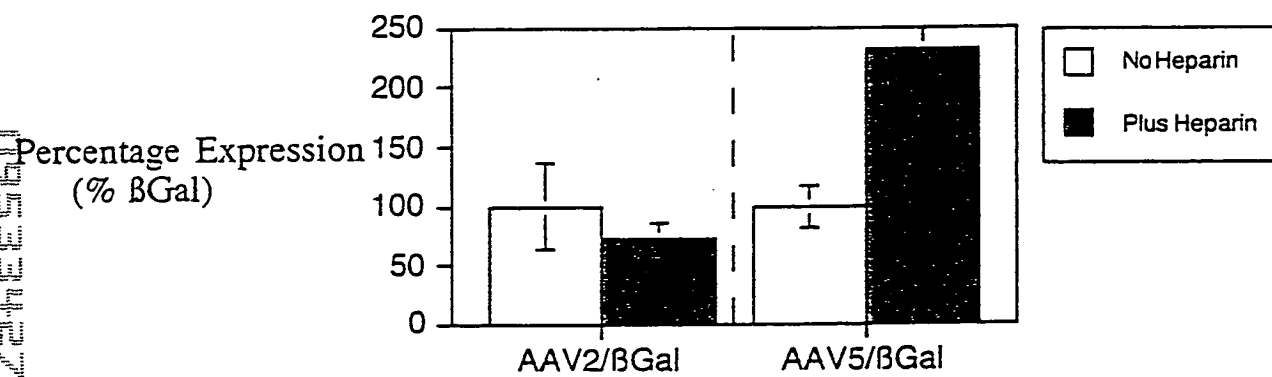


Fig. 19A

002220 032200 033427 03533427

β Gal Activity
(L.U./mgx10⁶)

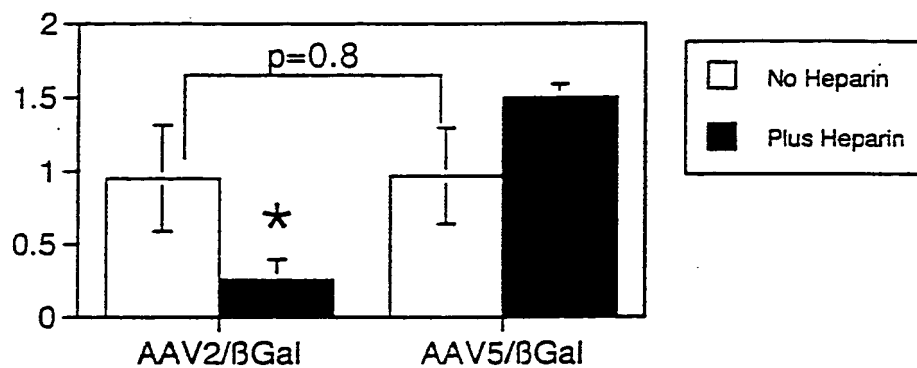


Fig. 19 B

00533427.032200

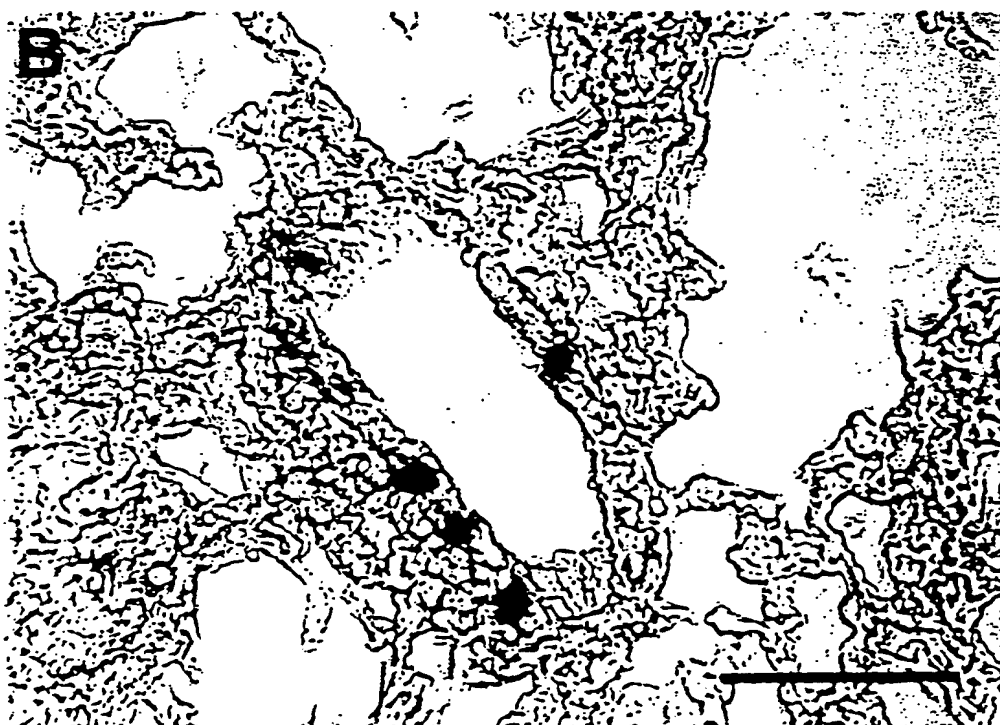
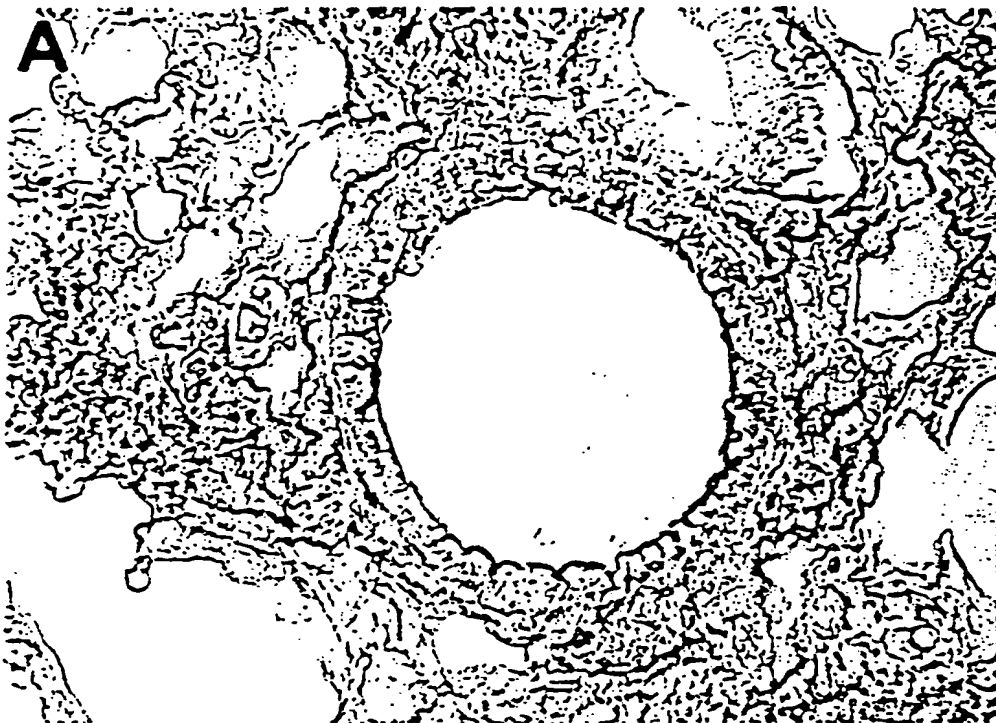


Fig 20 A+B

002220" 24E550

Blue Cells / field

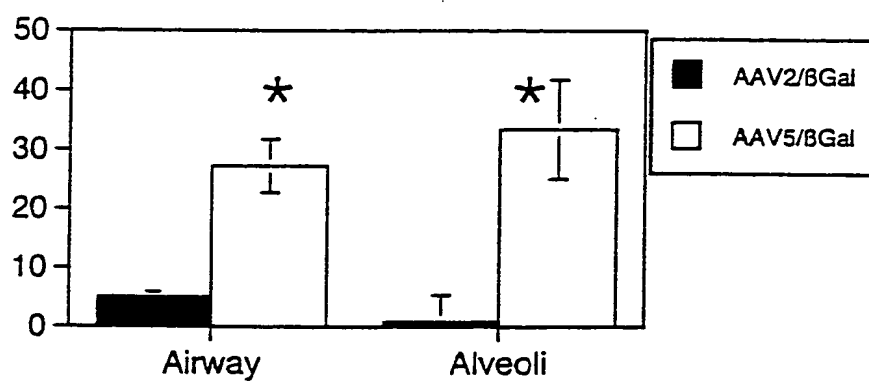


Fig 20C

09533427 032200

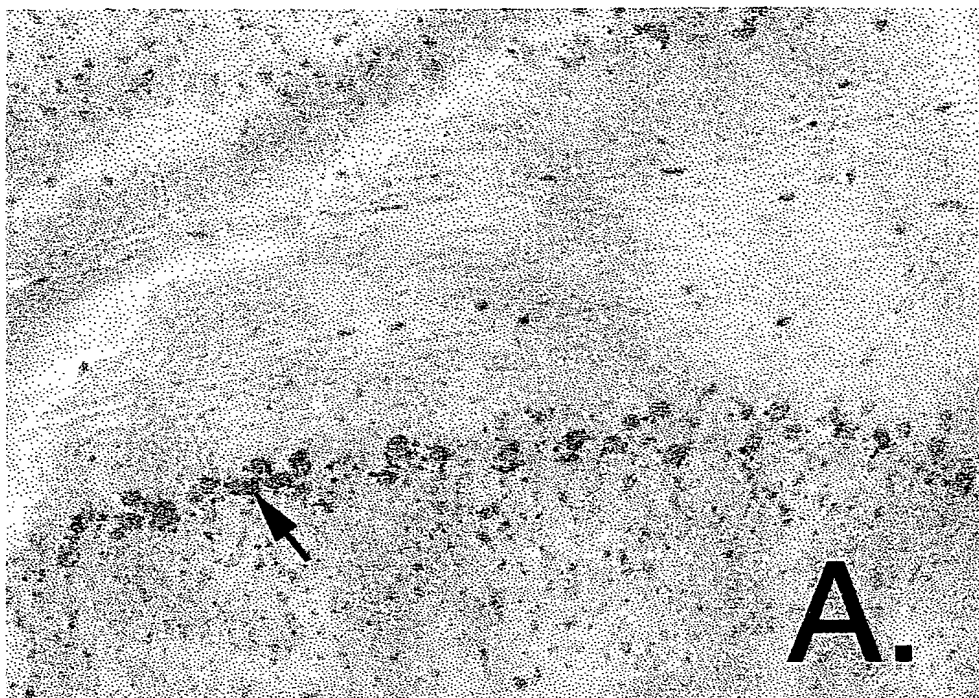
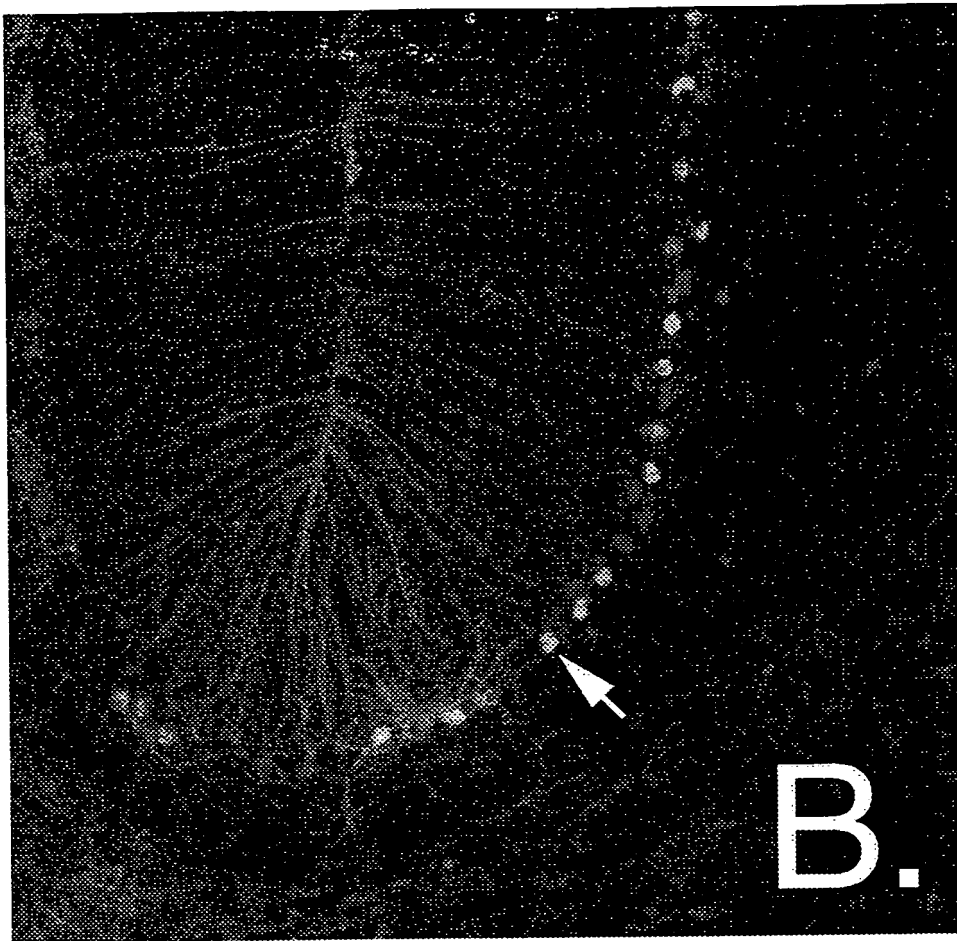
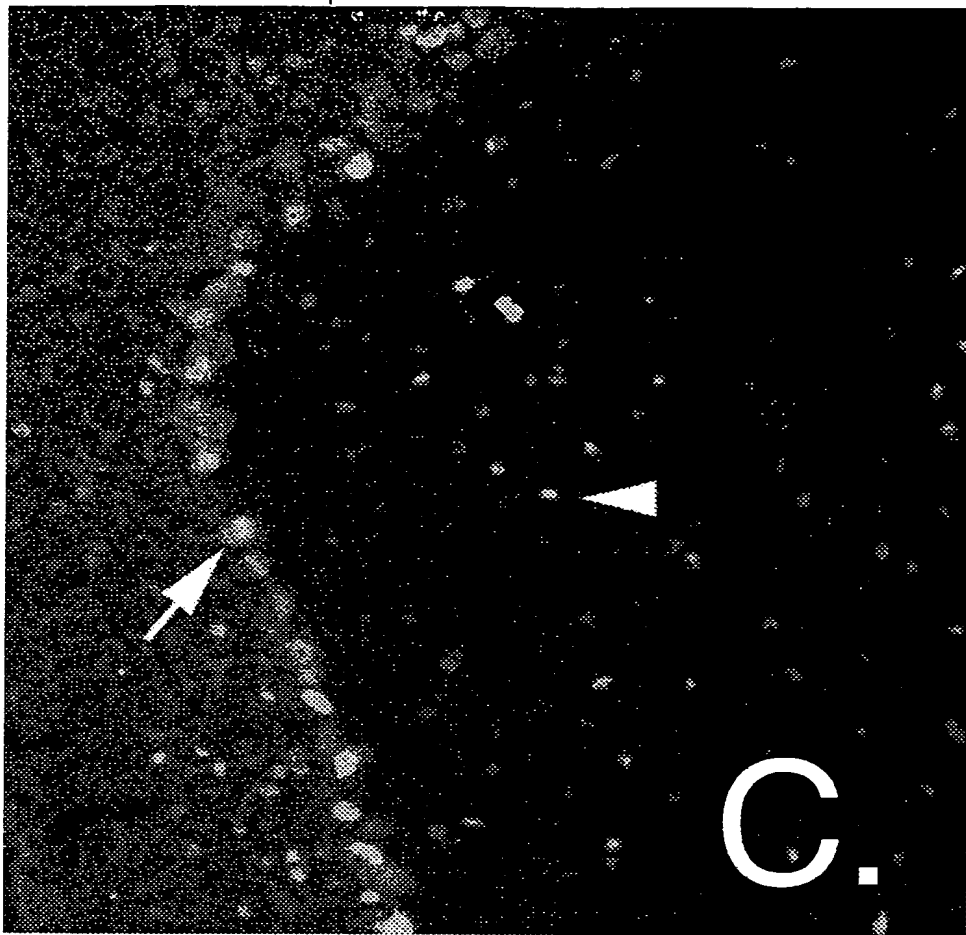


Fig. 21



002200

Fig. 22



00222E0

Fig 23